

Fig. 1

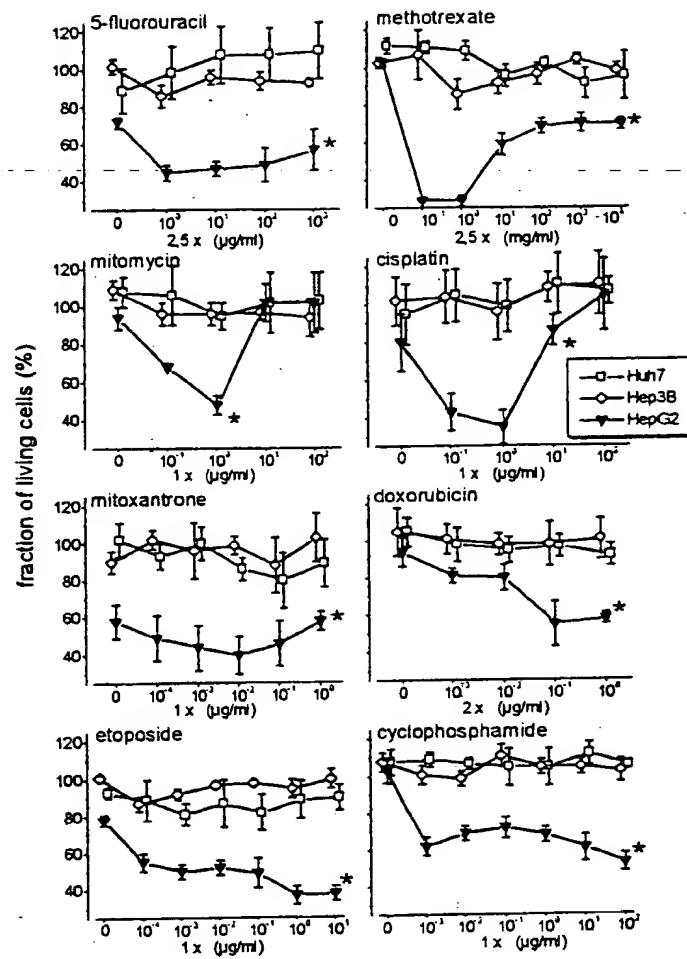


Fig. 2

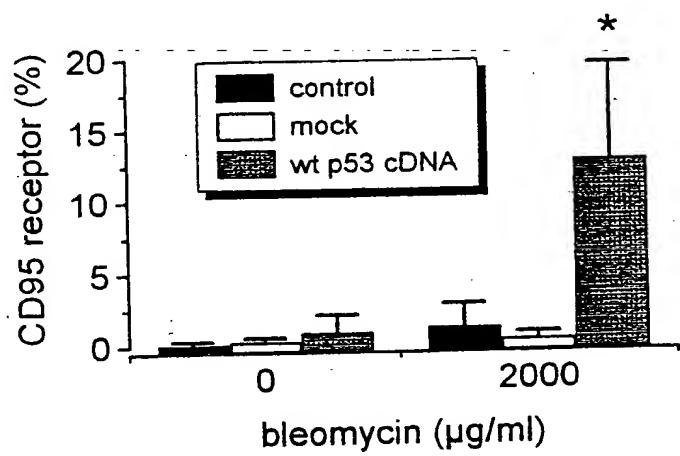


Fig. 3

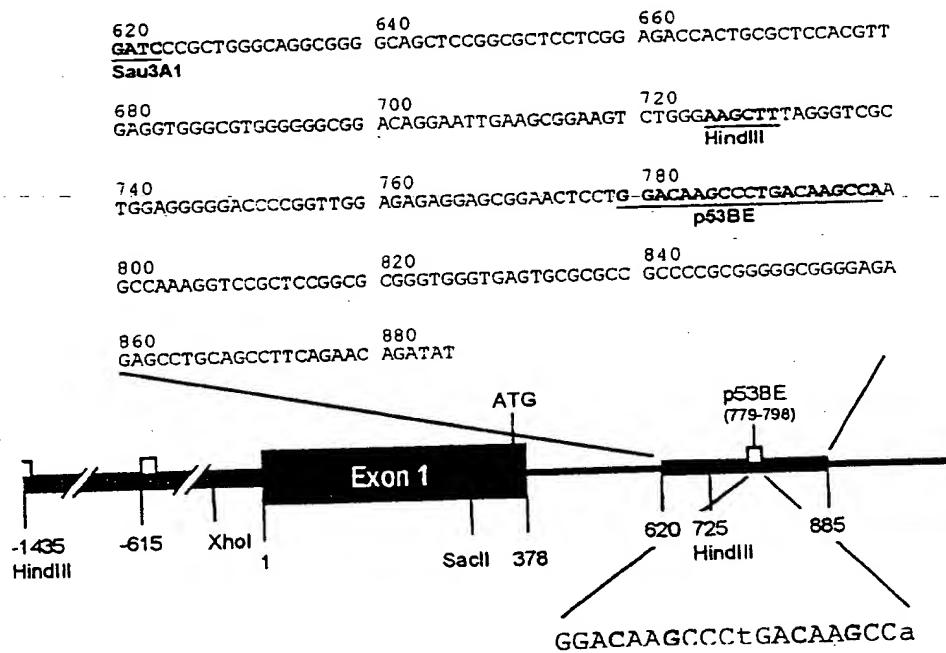


Fig. 4

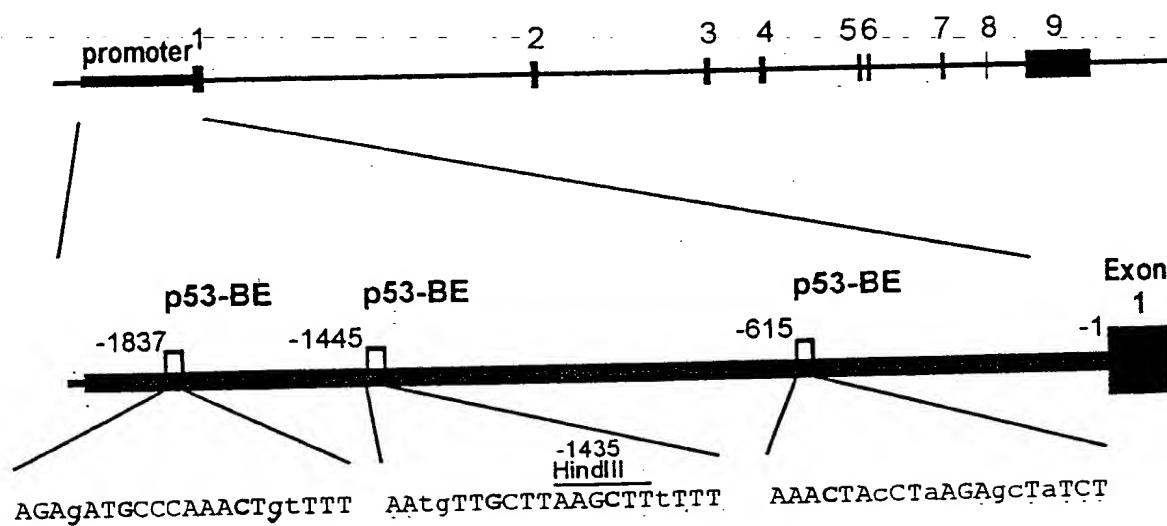


Fig. 5

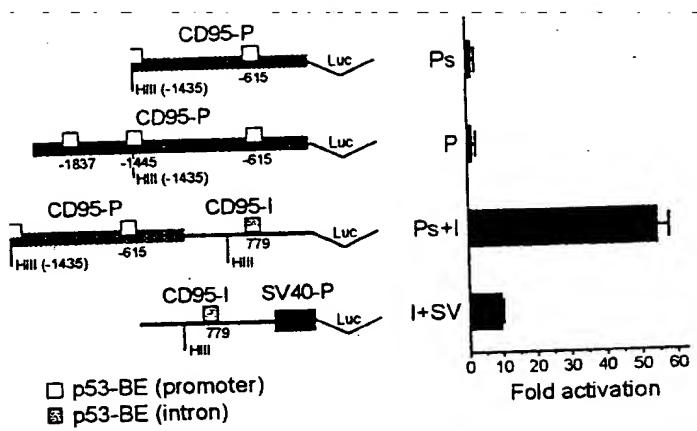


Fig. 6

1 GATCCCGCTGGCAGGCAGGAGCTCCGGCCTCTCGGAGACCACTGCGCTCCACGTT 60
1 CTAGGGCGACCGTCCGCCCGTCGAGGCCGAGGAGCCTCTGGTGACGCGAGGTGCAA
61 GAGGTGGCGTGGGGCGGACAGGAATTGAAGCGGAAGTCTGGAAAGCTTAGGGTCGC 120
61 CTCCACCCGCACCCCCCGCTGCTTAACCTCGCCTCAGACCCCTCGAAATCCCAGCG
121 <---- 4. P53-BE ---->
(intron)
121 TGGAGGGGACCCGGTTGGAGAGAGGAGCGGAACCTCTGGACAAAGCCCTGACAAAGCCAA 180
121 ACCTCCCCCTGGGGCAACCTCTCCTCGCCTGAGGACCTGTCGGGACTGTTCGGTT
181 GCCAAAGGTCCGCTCCGGCGGGTGGGTGAGTGCAGCCGCCCCGCGGGGGGGGAGA 240
181 CGGTTTCCAGGCAGGCCGCGCCACCCACTCACGCGCGGGCGGGCGCCCCCTCT
241 GAGCCTACAGCCTTCAGAACACATATTGCTCATTTCGAGTCTCAGACGTAGGAAA 300
241 CTCGGATGTCGGAAGTCTTGTGTATAACGAGTAAAAGACCGTCAAGAGTCTGCATCCTT
301 TAAGTCAGCACCGAAGCAGTGGTAAGCGGAGGGCTCGGAAGAACGGCACCTTTCTT 360
301 ATTCACTCGTGGCTTCGTACCAATTGGCCTCCGAGCCTCTGCCGTGGAAAAGAAA
361 CTCGAAAAAGTTATATGGGGCTGAATGAGCTCTGGAGGCTTACCGTTTTATT 420
361 GAGCTTTTCAATATACCCCCGACTTACTCGAAGACCTCCGAACAAATGGCAAAAATAA
421 GTCACACAGAAAAGGAAACTGCCTTGTCTCCCTCCGGAAATTCTCTTTAAGACTGTA 480
421 CAGTGTGTCTTCCCTTGACGGAACAGAGGGAGGCCCTTAAGAGAGAAAATTCTGACAT
481 AGTCGCTGCCTGAGTGGTTCATTTGTTCTGCCCTCTTTCTTTTG 540
481 TCAGCGACGGACTCACCAAAGTAAAACAAAACAAAAGACGGGAAGAGAAAGAAAAC
541 CCCTTCTTAGCTGCACTCCATGGTATTCTGCTTGGTCTCTGCTGGGTTGGTGG 600
541 GGGAAAGAATCGAACGTGAGGGTACCAACTAAAGACGAACCAGAGGACGACCCAAACC
601 TACTCGTCCCACCGCACAGAACCCGGCCTATTATTGCCAAGAAACTGAGCAGCCT 660
601 ATGAGCAAGGGTGGCGTGTCTGGGCCGCGATAATAACCGGTCTTGAACCGTGG
661 GTTTGAAAAGTCCCTCGCTCAGAAATGCCAGCTTGCAGATGGCTAATCAAAGAGACGTG 720
661 CAAAACTTTCAGGGAGCGAGTCTTACGGTCAACGTCTACCGATTAGTTCTCTGCAC

Fig. 8

2nd half of the

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(promoter)

	AGCTTTTGGCTACATTTTTATTTGAAAG	
448	-----+-----+-----+-----+-----+ 480	
	TCGAAAAACCGATGTAACAAACATTC	
481	TAAGTTAATAATCACTCATCTCACTGGCTATAATGATAAGTATTAAGTAAGGAAGATC ATTCAAATTATTAGTAGAGTAGACCGATATTACTATTATAATTCAATTCAATTCTCTAG	540
541	CACATATGTGAGTTGCTGGCTTATAATTCAACTCAAGAGATACTGATTTGTCATTG GTGTATACACTCAACGACCGAATATTAAGTGTGAGTTCTATGACTAAAACAGTTAAC	600
601	CCTTCCCCTTTTCTCTCTTCCCTCCATTCCCTTCCCTTACCTCTCCTTC GGAAAGGGGAAAAAAAGAGAGAAGGGAGGAAGGTAAAGGAAGAAGGGAAATGGAGAGGAAG	660
661	CTTCCCTCACACCCCTTTCTTCTTACATTTTTATTTAAATGAACCTTTC GAAGGGAGTGTGGGGAAAGGAAGGAAGAAAATGAAAAAAATAATTACTTGAAAG	720
721	ATTTGGAATAGTTAGGATTCAAAAAATTGCAAGAGATAATACAGAGAATGCCATA TAAAACCTTATCAAAATCCTAAAGTTAAACGTCTATTATGTCTTACGGGTAT	780
781	TACCATCCTTATCCCACCTCTTTGTGTCTATTAGATGTCAGAGTGTGACAA ATGGTAGGAGGAATAGGGTGAAGAAAAACACAGATAATCTACGAGTCTCACACACGTGTT	840
841	GGCTGGCACGCCAGGGCTTCCTCATGGCACTAACAGTCTACTGAAAGGTGGAACAGAG CCGACCGTGCAGGTCCAGAAGGGAGTACCGTGATTGTCAGATGACTTCCACCTGTCTC	900
901	ACAAGCCTATCAACACCTACAAGACTGGTGGTAAGTGCAGTGACAGATGCAAACACAGG TGTCGGATAGTTGGATGTTCTGACCACATTCACTGTCTACGTTGTGTC	960
991	GTGATGGAAAGCCCTCAGGAGGGTAACCTAACCTAGATTTGAGGGCCAAACAGGGCTCCA CACTACCTTCGGGAGTCCTCCATTGGATTGGATCTAAACTCCGGGTTGTCCGAGGT	1020
1021	GAAGAAAATGTCAACTGAGAGGAAGCCTGAAGGGATGAACAGTGGCTAAGCAAAGGGTTA CTTCTTTACAGTTGACTCTCCTCGGACTCCTACTTGTCAACCGATTGTTCCAAAT	1080

1081 TTAATGTGTATTAAATGGGTTGAATCTAATTGGGAAGGGAGAGAGGGTTGCAGAGTGAGGT
 1140 AATTACACATAATTACCCAACTTAGATTAACCCCTCCCTCTCTCCAACGTCTCACTCCA
 1141 GCAGAGCTTGGTGGACGATGCCAAGGAATACTGAAACCTTAGTGTGTCCAGTCTGGAA
 1200 CGTCTCGAACCAACCTGCTACGGTTCCCTATGACTTTGGAAATCACACAGGTAGACCT
 1201 CTGCATCCAAATTCAAGGTTCAAGTAATGATGTCATTATCAAACATACCTCTGTAAAATT
 1260 GACGTAGGTTAAAGTCCAAGTCATTACTACAGTAATAGGTTGTATGGAAGACATTTAA

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(promoter)

1261 CATGCTAAACTACCTAAGAGCTATCTACCGTTCAAAGCAATAGTGAACAGTGT
 1320 GTACGATTTGATGGATTCTCGATAGATGGCAAGGTTCGTTACTGAAACTTGTCA
 1321 TCACCAAGCACGAAAGAATTACAAGATTTTTAAAGAAAATTGCCAGGAAATAAT
 1380 AGTGGTCTCGTCTTCTTAATGTTCTAAAAAAAATTCTTTAACCGGTCTTTATTA
 1381 GAGTAACGAAGGACAGGAAGTAATTGTGAATGTTAATATAGCTGGGCTATGCGATTG
 1440 CTCATTGCTTCCTGTCCTTCATTAACACTACAAATTATATCGACCCCGATACGCTAAC
 1441 GCTTAAGTTGTTAGCTTGTGAGAAATAAAAACTAAGGGGCCCTCCCTTT
 1500 CGAATTCAACAATCGAAACAAAAGGAGAACTCTTATTTGATTCCCCGGGAGGGAAA
 1501 CAGAGCCCTATGGCGAACATCTGACTTTCATATGGTAACTGTCCATTCCAGGAAC
 1560 GTCTCGGGATACCGCGTTGTAGACATGAAAAGTATACCAATTGACAGGTAAGGTCTTG
 1561 GTCTGTGAGCCTCTCATGTTGCAGCCACAACATGGACAGCCCAGTCAAATGCCCGCAAG
 1620 CAGACACTCGGAGAGTACAACGTCGGTGTGTACCTGTCGGTCAGTTACGGGGCGTTC
 1621 TCTTCTCTGAGTGAETCCAGCAATTAGCCAAGGCTCTGTACCCAGGCAGGACCTCTGC
 1680 AGAAAGAGACTCACTGAGGTCGTTAATCGGTTCCGAGGACATGGTCCGTCTGGAGACG
 1681 GCTCTGAGCTCCATTCTCTTCAAGACCTCCCCAACTTCCAGGTTGAACATACAGCAGAA
 1740 CGAGACTCGAGGTAAGAGGAAGTCTGGAGGGGTTGAAGGGTCCAACTTGATGTCGTCTT
 1741 GCCTTAGAAAGGGCAGGAGGCCGGCTCGAGGTCTCACCTGAAGTGAGCATGCCAGC
 1800 CGGAAATCTTCCGCTCCGGCCGAGAGCTCCAGGAGTGGACTCACTCGTACGGTC
 1801 CACTGCAGGAACGCCCGGGACAGGAATGCCATTGTGCAACGAACCTGACTCCTTCC
 1860 GTGACGTCTTGCGGGGCCCTGTCCTTACGGTAAACACGTTGCTGGACTGAGGAAGG
 1861 TCACCCCTGACTTCTCCCCCTCCCTACCCGCGCGCAGGCCAAGTTGCTGAATCAATGGAGC
 1920 AGTGGGACTGAAGAGGGGAGGGATGGCGCGTCCGGTTAACGACTTAGTTACCTCG

1921 CCTCCCCAACCGGGCGTTCCCCAGCGAGGCTTCCTCCATCCTCCTGACCACCGGGGC
1980 GGAGGGGTTGGGCCCCGCAAGGGGTGCTCCGAAGGAAGGGTAGGAGGACTGGTGGCCCCG
1981 TTTTCGTGAGCTCGTCTGTGATCTCGCGCAAGAGTGACACACAGGTGTTCAAAGACGCTT
2040 AAAAGCACTCGAGCAGAGACTAGAGCGCGTCTCACTGTGTGTCACAAGTTCTCGCAA
2041 CTGGGGAGTGAGGGAAAGCGGTTACGAGTGACTTGGCTGGAGCCTCAGGGCGGGCACTG
2100 GACCCCTCACTCCCTCGCAAATGCTACTGAACCGACCTCGGAGTCCCCGCCGTGAC
2101 GCACGGAACACACCCCTGAGGCCAGCCCTGGCTGCCAGGCGGAGCTGCCTTTCTCCGC
2160 CGTGCCTTGTGTGGGACTCCGGTCGGGACCGACGGGTCCGCCTCGACGGAGAAGAGGGCG
2161 GGACATGTACAGAGCTCGAGAAGTACTAGTGGCACGTGGCCGTGACCTTAAGCTTA
2220 CCTGTACATGTCTCGAGCTCTCATGATCACCGGTGCACCGGGCACGTGGAATTGAAAT

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2221 GGGTCGCTGGAGGGGGACCCCGGTTGGAGAGAGGGAGCGGAACCTCTGGACAAGCCCTGAC
2280 CCCAGCGACCTCCCCCTGGGCCAACCTCTCTCGCCTTGAGGACCTGTTGGGACTG

----→

2281 AAGCCAAGCAAAGGTCCGCTCCGGCGCGGGTGGGTGAGTGCGCGCCGCCCGGGGGC
2340 TTCCGGTTCGGTTCCAGGCAGGGCGGCCACCCACTCAGCGCGGGCGGGCGCCCCCG
2341 GGGGAGAGAGCCTGCAGCCTCAGAACAGATATTGCTCATTTCAGGCAGTTCTCAGACG
2400 CCCCTCTCTCGGACGTGGAAAGTCTGTCTATAACGAGTAAAGACCGTCAAGAGTCTGC
2401 TAGGAAATAAGTCAGCACCGAACGAGTGGTTAACGCCGGAGGGCTCGGAAGAACGGCACCT
2460 ATCCTTTATTCAAGTCGTGGCTTCGTCACCAATTGGCCTCCGAGCCTTGTGCCGTGGA
2461 TTTCTTCTCGAAAAAGTTATATGGGGCTGAATGAGCTCTGGAGGCTTGTACCGTT
2520 AAAGAAAGAGCTTTCAATATAACCCCCGACTTACTCGAACGACCTCCGAACAAATGGCAA
2521 TTTTATTGTACACAGAAAAGGAAACTGCCTTGTCTCCCTCGGAAATTCTCTCTTTAA
2580 AAAATAACAGTGTGTTCTTGCCTTGACGGAACAGAGGGAAAGGCCCTTAAGAGAGAAATT
2581 GACTGTAAGTCGCTGCCTGAGTGGTTTCAATTGTTGTTCTGCCCTCTCTTTCT
2640 CTGACATTCAAGCGACGGACTCACCAAAGTAAAACAAAAGACGGGAAGAGAAAGA
2641 TCTTTGCCCTTCTTAGCTTGCACTCCATGGTATTCTGCTTGGTCTCTGCTGGGG
2700 AGAAAACGGGAAAGAACGAAACGTGAGGGTACCAACTAAAGACGAACCAGAGGGACGACCCC

Fig. 8 (cont'd III)

2701 TTGGTGGTACTCGTCCCACCGCACAGAACCCGGCGCTATTATTGGCCAAGAAACTTGA
AACCACCATGAGCAAGGGTGGCGTCTGGGCCGGATAATAACCGGTTCTTGAAC
2760
2761 GCAGCCTGTTGAAAAGTCCCTCGCTCAGAAATGCCAGCTGCAGATGGCTAATCAAAG
CGTCGGACAAAACCTTTCAAGGGAGCGAGTCTTACGGTCAACGTCTACCGATTAGTTTC
2820
2821 AGACGTG
2827 TCTGCAC

Fig. 9

<---- 1.p53-BE --

1 TGAGGACTCTAGGAATATGCTGGTAAAATAACCTTAGAGATGCCAACTGT
 1 ACTCCTGAGAGTCCTTATACGACCATTATTTATTGAAATCTCTACGGGTTGACA 60
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 61 TTTCCCCAGAACACCAGCATTCAATTAGGTGTTCAATTCAATAGATTCTCAAAGGATTCCA
 61 AAAGGGGTCTTGTGGTCGTAAGTAATCCACAAGTAAGTTATCTAAGAAGTTCTAAGGT 120
 121 AAGGCAAAGAAGTTGGGGAACAGTATATATAATTACCAACCCCTTGACATTAGCATA 180
 121 TTCCGTTCTCAAACCCCTGTCAATATATAATTAAATGGGTGGGAACTGTAATCGTATG
 181 TAAGGGCCCTGAGAAGTTGGATTAAGAAAGTTCAAATTAAAGTAACCCAGAATT 240
 181 ATTCCCGGGACTCTCAAAACCTAATTCTCAAAAGTTAATTCAATTGGGTCTTAAA
 241 CTAAGATTATTGACCATGAAACATATGTCCTTCAACAAAGCACATATTCTATCTCCTT 300
 241 GATTCTAATAAACTGGTACTTGTATACAGAGGGGTGTTCGTGATAAGGATAGAGGAA
 301 GAACTTGAGGATAATTAGACGTACGTGGTAGAGGGTAGGGGAAGGGGTATGGCATAGA 360
 301 CTTGAECTCCTATTAATCTGCATGCACCCATCTCCATCCCCCTCCCCATACCGTATCT
 361 AAGAGCAGGACCTTGGAGCAAGAATATCTAAGTTAATTCTGACTCTGCTATTATTA 420
 361 TTCTCGTCCTGAAACCCCTGTTCTATAGATTCAAATTAGGACTGAGACGATAATAAT

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 421 TGATTGGTAGAACGGTTACAACGAATTGAAAAACCGATGTAACAAACATTTC
 481 TAAGTTAATAATCACTCATCTCACTGGCTATAATGATAAGTATTAAGTAAGGAAGATC 540
 481 ATTCAAATTATTAGTGAGTAGAGTGACCCGATATTACTATTCTAATTCTCCTCTAG
 541 CACATATGTGAGTTGCTGGCTTATAATTCAACTCAAGAGATACTGATTTGTCAATTGT 600
 541 GTGTATACACTCAACGACCGAATTAAAGTGTGAGTTCTATGACTAAACAGTTAAC
 601 CCTTCCCCCTTTTCTCTCTCCCTCCTCCATTCCCTTCCCTTACCTCTCCTTC 660
 601 GGAAAGGGAAAAAAAGAGAGAAGGGAGGAAGGTAAGGAAGGAATGGAGAGGAAAG

661 CTTCCCTCACACCCCTTCTCTTACATTTTATTTAAATGAACCTTTC
 GAAGGGAGTGTGGGAAAAGGAAGGAAGAAAATGTAAAAAATAAATTACTGAAAAG 720

721 ATTTGGAATAGTTAGGATTCAAAAATTGCAGAGATAATACAGAGAATGCCATA
 TAAAACCTTATCAAATCCTAAAGTTTAAACGTCTATTATGTCTTACGGGTAT 780

781 TACCATCCTCTTATCCACTCTTTGTCTATTAGATGCTCAGAGTGTGCACAA
 ATGGTAGGAGGAATAGGGTGAAGAAAACACAGATAATCTACGAGTCTCACACACGTGTT 840

841 GGCTGGCACGCCAGGGCTTCCTCATGGCACTAACAGTCTACTGAAAGGTGGAACAGAG
 CCGACCGTGCAGGTCCCCAGAAGGAGTACCGTGATTGTAGATGACTTCCACCTGTCTC 900

901 ACAAGGCTATCAACACCTACAAGACTGGTGGTAAGTGCAGTGACAGATGCAAAACACAGG
 TGGTCGGATAAGTGTGGATGTTCTGACCACATTACGTCACTGTCTACGTTGTGTC 960

991 GTGATGGAAAGCCCTCAGGAGGGTAACCTAACCTAGATTGAGGGCCAAACAGGCTCCA
 CACTACCTTCGGGAGTCCTCCCATTGGATTGGATCTAAACTCCCGGTTGTCCGAGGT 1020

1021 GAAGAAAATGTCAACTGAGAGGAAGCCTGAAGGATGAACAGTGGCTAAGCAAAGGGTA
 CTTCTTTACAGTTGACTCTCCTCGGACTTCACTGTCAACCGATTGTTCCCAAT 1080

1081 TTAATGTGTTATTAAATGGGTTGAATCTAATTGGGAAGGGAGAGAGGTTGCAGAGTGAGGT
 AATTACACAAATAATTACCCAACTTAGATTAAACCTTCCCTCTCTCAACGTCTCACTCCA 1140

1141 GCAGAGCTTGGTGGACGATGCCAAGGAATACTGAAACCTTGTGTCCAGTCTGGAA
 CGTCTCGAACCAACCTGCTACGGTTCCCTATGACTTGGAAATCACACAGGTGAGACCTT 1200

1201 CTGCATCCAAATTCAAGGTTCACTGATGTCATTATCAAACATACCTCTGTAAAATT
 GACGTAGGTTAAGTCAAGTCATTACTACAGTAATAGGTTGTATGGAAGACATTAA 1260

<---- 3.p53-BE ---->

1261 CATGCTAAACTACCTAACAGAGCTATCTACCGTTCCAAAGCAATAGTGAACAGTGT
 GTACGATTGATGGATTCTCGATAGATGGCAAGGTTCGTTATCACTGAAACTGTCA 1320

1321 TCACCAAGCACGAAAGAATTACAAGATTTTTAAAGAAAATTGCCAGGAAATAAT
 AGTGGTCTCGTCTTCTTAATGTTCTAAAAAAATTCTTTAACCGGTCTTATTAA 1380

1381 GAGTAACGAAGGACAGGAAGTAATTGTGAATGTTAATATAGCTGGGCTATGCGATTG
 CTCATTGCTCCTGTCCTTCATTAACACTACAAATTATATCGACCCCCGATACGCTAAC 1440

1441 GCTTAAGTTGTTAGCTTGTCTTCTGAGAAATAAAACTAAGGGCCCTCCCTTT
 CGAATTCAACAATCGAAACAAAGGAGAACTCTTATTTGATCCCCGGGAGGGAAA 1500

1501 CAGAGCCCTATGGCGCAACATCTGTACTTTCATATGGTTAATGTCCATTCCAGGAAC
 GTCTCGGGATACCGCGTTGTAGACATGAAAAGTATACCAATTGACAGGTAAGGTCTTG 1560

1561 GTCTGTGAGCCTCTCATGTTGAGCCACAAACATGGACAGCCAGTCAAATGCCCGCAAG 1620
 CAGACACTCGGAGAGTACAACGTCGGTGTACCTGTCGGTCAGTTACGGGGCGTTC

 1621 TCTTTCTCTGAGTGACTCCAGCAATTAGCCAAGGCTCTGTACCCAGGCAGGACCTCTGC 1680
 AGAAAGAGACTCACTGAGGTCGTTAACCGGTCAGGACATGGGTCGTCGGAGACG

 1681 GCTCTGAGCTCCATTCTCCTCAAGACCTCCCCAACTTCCCAGGTTGAACCTACAGCAGAA 1740
 CGAGACTCGAGGTAAGAGGAAGTTCTGGAGGGTTGAAGGGTCCAACTTGATGTCGTCTT

 1741 GCCTTAGAAAGGGCAGGAGGCGGCTCTGAGGTCTCACCTGAAGTGAGCATGCCAGC 1800
 CGGAAATCTTCCCGTCTCCGGCGAGAGCTCCAGGAGTGGACTCACTCGTACGGTCG

 1801 CACTGCAGGAACGCCCGGGACAGGAATGCCATTGCAACGAACCTGACTCCTCC 1860
 GTGACGTCCCTGCGGGCCCTGTCCTTACGGTAAACACGTTGCTGGGACTGAGGAAGG

 1861 TCACCCCTGACTTCTCCCCCTCCCTACCCGCGCGCAGGCCAAGTTGCTGAATCAATGGAGC 1920
 AGTGGGACTGAAGAGGGGGAGGGATGGCGCGTCCGGTTCAACGACTTAGTTACCTCG

 1921 CCTCCCCAACCCGGGCGTTCCCCAGCGAGGTTCCCTCCATCCTCTGACCACCGGGGC 1980
 GGAGGGGTTGGGCCCCGAAGGGTCGCTCGAAGGAAGGGTAGGAGGACTGGTGGCCCCG

 1981 TTTTCGTGAGCTCGTCTTGATCTCGCGAAGAGTGACACACAGGTGTTCAAAGACGCTT 2040
 AAAAGCACTCGAGCAGAGACTAGAGCGCGTCTCACTGTGTCCACAAGTTCTGCGAA

 2041 CTGGGGAGTGAGGGAAAGCGGTTACGAGTGACTGGCTGGAGCCTCAGGGCGGGCACTG 2100
 GACCCCTCACTCCCTCGCAAATGCTCACTGAACCGACCTCGGAGTCCCCGCGTGCAC

 2101 GCACGGAACACACCCCTGAGGCCAGCCCTGGCTGCCAGGGCGAGCTGCCTTTCTCCGC 2160
 CGTGCCTTGTGTGGACTCCGGTGGGACCGACGGTCCGCCCTGACGGAGAAGAGGGCG

 2161 GGACATGTACAGAGCTCGAGAAGTACTAGTGGCACGTGGCCGTGCACCTTAAGCTTA 2220
 CCTGTACATGTCTCGAGCTTTCATGATCACCGGTGCACCCGGCACGTGGAATTGAAAT

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 (intron)

 2221 GGGTCGCTGGAGGGGACCCCGGTTGGAGAGAGGGAGCGGAACCTCTGGACAAGCCCTGAC 2280
 CCCAGCGACCTCCCCCTGGGCAACCTCTCCTCGCCTTGAGGACCTGTCGGGACTG

 ----->

 2281 AAGCCAAGCCAAGGTCCGCTCCGGCGGGTGGTGAGTGCAGGCCGCCGGCGGGGC 2340
 TTCCGGTTCGGTTCCAGGCGAGGCCGCCACCCACTCACGCGCGGGCGCCCG

 2341 GGGGAGAGAGCCTGCAGCCTTCAGAACAGATATTGCTCATTTCTGGCAGTTCTCAGACG 2400
 CCCCTCTCTCGGACGTCGGAAGTCTGTCTAACGAGTAAAGACCGTCAAGAGTCTGC

TAGGAAATAAGTCACACCGAACAGTGGTTAAGCCGGAGGGCTCGGAAGAACGGCACCT
 2401 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 2460
 ATCCTTATTCACTCGTGGCTTCGTACCAATTGGCCTCCGAGCCTTGTGCCGTGGA

 TTTCTTCTCGAAAAAGTTATATGGGGCTGAATGAGCTTCTGGAGGCTTGTACCGTT
 2461 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 2520
 AAAGAAAGAGCTTTCAATATAACCCCCGACTTACTCGAACCTCCGAACAAATGGCAA

 TTTTATTGTCACACAGAAAAGGAAACTGCCTTGTCTCCCTTCCGGAAATTCTCTCTTAA
 2521 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 2580
 AAAATAACAGTGTGCTTTCCCTTGACGGAACAGAGGAAAGGCCCTAACAGAGAGAAATT

 GACTGTAAGTCGCTGCCTGAGTGGTTCATTTGTTTGTCTGCCCTCTCTTCT
 2581 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 2640
 CTGACATTCAAGCAGGACTCACCAAAAGTAAAACAAAAGACGGAAAGAGAAAGA

 TCTTTGCCCTTCTAGCTGACTCCATGGTATTCTGCTTGGTCTCTGCTGGG
 2641 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 2700
 AGAAAACGGAAAGAACGTGAGGGTACCACTAAAGACGAACCAGAGGACGACCCC

 TTGGTGGTACTCGTCCACCGCACAGAACCCGGCGCTATTATTGCCAAGAAACTTGA
 2701 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 2760
 AACCAACCATGAGCAAGGGTGGCGTGTCTGGGCCGCGATAATAACCGTTCTTGAAC

 GCAGCCTGTTGAAAAGTCCCTCGCTCAGAAATGCCAGCTGCAGATGGCTAATCAAAG
 2761 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 2820
 CGTCGGACAAAACTTTCAGGGAGCGAGTCTTACGGTCAACGTCTACCGATTAGTT

 AGACGTG
 2821 ----- 2827
 TCTGCAC

Fig. 10

<---- 1.p53-BE ----
(promoter)

1 TGAGGACTCTAGGAATATGCTGGAAAATAACCTTAGAGATGCCAAACTGT 60
 1 ACTCTGAGAGTCCTTATACGACCATTATTTATTGGAAATCTCTACGGGTTGACA
 -->
 61 TTTCCCCAGAACACCAAGCATTCAATTAGGTGTCATTCAATAGATTCTCAAAGGGATTCCA 120
 61 AAAGGGGTCTTGTGGTCGTAAGTAATCCACAAGTAAGTTATCTAAGAAGTTCTAAGGT
 121 AAGGCAAAGAAGTTGGGAACAGTATATATAATTACCAACCCCTTGACATTAGCATA 180
 121 TTCCGTTCTCAAACCCCTTGTCAATATATAATTGGTTGGAAACTGTAATCGTATG
 181 TAAGGGCCCTGAGAAGTTGGATAAGAAAGTTCAAATTAAAGTAACCCAGAATTT 240
 181 ATTCCCAGGACTCTCAAAACCTAATTCTCAAAGTTAATTCAATTGGTCTAAAAA
 241 CTAAGATTATTGACCATGAAACATATGTCCTTACAAAGCACATATTCTATCTCCTT 300
 241 GATTCTAATAAACTGGTACTTGTATACAGAGGGGTGTTCGTGTATAAGGATAGAGGA
 301 GAACTTGAGGATAATTAGACGTACGGTAGAGGGTAGGGGAAGGGGTATGGCATAGA 360
 301 CTTGAACCTCTATTAACTGCATGCACCCATCTCCATCCCTCCCCATACCGTATCT
 361 AAAGAGCAGGACCTTGGGAGCAAGAATATCTAAGTTAATTCTGACTCTGCTATTATA 420
 361 TTCTCGTCTGGAACCCCTCGTTTATAGATTCAAATTAAAGGACTGAGACGATAAAATAT

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(promoter)

421 ACTAACCATCTTGCCAATGTTGCTTAAGCTTTGGCTACATTTTTATTGTAAAG 480
 421 TGATGGTAGAACGGTTACAAACGAATTGGAAAAACCGATGTAACAAACATTTC
 481 TAAGTTAATAATCACTCATCTACTGGCTATAATGATAAGTATTAAGTAAGGAAGATC 540
 481 ATTCAAATTATTAGTGAGTAGGTGACCCGATATTACTATTCTAATTCTCTCTAG
 541 CACATATGTGAGTTGCTGGCTATAATTCAACTCAAGAGATACTGATTTGTCAATTGT 600
 541 GTGTATACACTCAACGACCGAATTAAAGTGTGAGTTCTATGACTAAACAGTTAAC
 601 CCTTTCCCTTTCTCTCTCCCTCCATTCTCTCCCTACCTCTCTTC 660
 601 GGAAAGGGAAAAAAAGAGAGAAGGGAGGAAGGTAAGGAAGAAGGAATGGAGAGGAAAG
 661 CTTCCCTCACACCCCTTCTCTCTTACATTTTTATTAAATGAACTTTTC 720
 661 GAAGGGAGTGTGGGAAAAGGAAGGAAGAAAATGTAAAAAAATTAATTGAAAG
 721 ATTTGGAATAGTTAGGATTCAAAAATTGCAAGAGATAATACAGAGAATGCCATA 780
 721 TAAACCTTATCAAAATCTAAAGTTAAACGTCTATTATGTCCTACGGGTAT

Fig. 10 (cont'd I)

781 TACCATCCTCCTTATCCCACTTCTTTGTCTATTAGATGCTCAGAGTGTGCACAA + 840
 ATGGTAGGAGGAATAGGGTGAAGAAAAACACAGATAATCTACGAGTCTCACACACGTGTT
 841 GGCTGGCACGCCAGGGCTTCCTCATGGCACTAACAGTCTACTGAAAGGTGAAACAGAG + 900
 CCGACCGTGGGGTCCCAGAAGGAGTACCGTATTGTCAGATGACTTCCACCTGTCTC
 901 ACAAGCCTATCAACACCTACAAGACTGGTGGTAAGTGCAGTGACAGATGCAAACACAGG + 960
 TGTCGGATAGTTGGATGTTCTGACCACATTACGTCACTGTCTACGTTGTGTC
 961 GTGATGGAAAGCCCTCAGGAGGGTAACCTAACCTAGATTGAGGGCCAAACAGGCTCCAG + 1020
 CACTACCTTCGGGAGTCCCTCCATTGGATTGGATCTAAACTCCGGTTGTCCGAGGTC
 1021 AAGAAAATGTCACGTGAGAGGAAGCCTGAAGGATGAACAGTGGCTAACCAAAGGTTAT + 1080
 TTCTTTACAGTTGACTCTCCTCGGACTTCTACTTGTCAACCGATTGTTCCAAATA
 1081 TAATGTGTTATTAATGGGTGAATCTAATTGGAAAGGGAGAGAGGTTGCAGAGTGAGGTG + 1140
 ATTACACAATAATTACCCAACCTAGATTAACCCCTCCCTCTCCAACGTCTCACTCCAC
 1141 CAGAGCTTGGTGGACGATGCCAAGGAATACTGAAACCTTAGTGTGTCCAGTCTGAAAC + 1200
 GTCTCGAACCCACCTGCTACGGTTCTTATGACTTGGAAATCACACAGGTAGACCTTG
 1201 TGCATCCAATTCAAGGTTAGTAATGATGTCTTACCCAAACATACCTTCTGAAAATTG + 1260
 ACGTAGGTTAAGTCCAAGTCATTACTACAGTAATAGGTTGTATGGAAGACATTTAAG

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(promoter).

1261 ATGCTAAACTACCTAAGAGCTATCTACCGTCCAAAGCAATAGTGAACAGTGT + 1320
 TACGATTGATGGATTCTCGATAGATGGCAAGGTTCTTATCACTGAAACTTGTCAACAA
 1321 CACCAAGGACACGAAAGAATTACAAGATTTTTAAAGAAAATGCCAGGAAATAATG + 1380
 GTGGTCTCGTCTTCTTAATGTTCTAAACGGTCTTTTATTAC
 1381 AGTAACGAAGGACAGGAAGTAATTGTGAATGTTAATATAGCTGGGCTATGCGATTGG + 1440
 TCATTGCTTCCGTCTTCATTAAACACTACAAATTATCGACCCCGATACGCTAAACC
 1441 CTTAAGTTGTTAGCTTCTTCTTGAGAAATAAAACTAAGGGCCCTCCCTTTC + 1500
 GAATTCAACAATCGAAACAAAAGGAGAACCTTTTATTTGATTCCCCGGAGGGAAAAG
 1501 AGAGCCTATGGCGAACATCTGACTTTCTATGTTAACGTCCATTCCAGAAACG + 1560
 TCTCGGAATACCGCGTTGTAGACATGAAAAGTATACCAATTGACAGGTAAAGGTCTTGC
 1561 TCTGTGAGCCTCTCATGTTGCAGCCACACATGGACAGCCAGTCACATGCCCGCAAGT + 1620
 AGACACTCGGAGAGTACAACGTCGGTGTACCTGTCGGGTCACTTACGGGGCGTTCA
 1621 CTTTCTGAGTGACTCCAGCAATTAGCCAAGGCTCTGTACCCAGGCAGGACCTCTGCG + 1680
 GAAAGAGACTCACTGAGGTGTTAACCGTTCCGAGGACATGGTCCGTCTGGAGACGC
 1681 CTCTGAGCTCCATTCTCCTCAAGACCTCCCAACTTCCAGGTTGAACATACAGCAGAAG + 1740
 GAGACTCGAGGTAAAGAGGAAGTTCTGGAGGGTTGAAGGGTCCAACTTGATGTCGTCTC

1741 CCTTAGAAAGGGCAGGAGGCCGGCTCGAGGTCCACCTGAAGTGAGCATGCCAGCC 1800
 GGAAATCTTCCCGTCTCCGGCCAGAGCTCAGGAGTGGACTCACTGTACGGTCGG
 ACTGCAGGAACGCCCCGGGACAGGAATGCCATTGIGCAACGAACCTGACTCCTCC 1860
 1801 TGACGTCTTGCGGGGCCCTGTCTTACGGTAAACACGTTGCTGGACTGAGGAAGGA
 CACCCTGACTCTCCCCCTCCCTACCCGGCCAGGCCAAGTTGCTGAATCAATGGAGCC 1920
 1861 GTGGGACTGAAGAGGGGGAGGGATGGCGCGTCCGGTCAACGACTTAGTTACCTCGG
 CTCCTCAACCCGGGCGTCTCCCAGCGAGGCTTCCATCCCTGACCACCGGGCT 1980
 1921 GAGGGGTTGGCCCGCAAGGGGTGCTCCGAAGGAAGGGTAGGAGGACTGGTGGCCCCGA
 TTTCGTGAGCTCGTCTGATCTCGCGCAAGAGTGACACACAGGTGTTCAAAGACGCTTC 2040
 1981 AAAGCACTCGAGCAGAGACTAGAGCGCTTCACTGTGTGTCACAAGTTCTGCGAAG
 TGGGGAGTGAGGGAAAGCGGTTACGAGTGACTGGCTGGAGCCTAGGGCGGGACTGG 2100
 2041 ACCCCTCACTCCCTCGCAAATGCTCACTGAACCGACCTCGGAGTCCCCGCCGTGACC
 CACGGAACACACCCCTGAGGCCAGCCCTGGCTGCCAGGGAGCTGCCCTCTCCCGCG 2160
 2101 GTGCCTTGTGTGGACTCCGGTCCGGACCGACGGGTCCGCCCGACGGAGAAGAGGGCGC
 GGTTGGTGGACCCGCTCAGTACGGAGTTGGGAAGCTTTCACTCGGAGGATTGCTCA 2220
 2161 CCAACCACCTGGCGAGTCATGCCCAACCCCTCGAGAAAGTGAAGCCTCTAACGAGT
 ACAACCATGCTGGCATCTGGACCCCTCACCTCTGGTATCCCCTCTGCCCGGGTGG 2280
 2221 TGTTGGTACGACCGTAGACCTGGAGGATGGAGACCACTAGGGAGAGGACGGCCACC
 AGGCTTACCCGTCTAGTCCCCGGATAGGCAAAGTGGGGCGGGCGCGGTGCG 2340
 2281 TCCGAATGGGCAGAATCAGGGCCCTATCCGTTACCCCGCCCGCCCTGCGCACGC
 GGATTGCGCGGCAGCGCGCACGCCACCTGGAGCGGGCTGCTGCGGGAGGCG 2400
 2341 CCTAACGCCCGTCCGGCGTGCACCGTGGACCCCTCGCCGCCGACGACGCCCTCCGC
 TTGGAGACTGGCTCCGGGGCTGTTAGGACCTCCCTCAGGCCGGTGTCAAGAACGA 2460
 2401 AACCTCTGACCGAGGGCCCCGACAATCTGGAAGGGAGTCCGGGCCACGAGTCTTGCT
 TGGAGGACTTGCTTTCTGGGCTTGATGCGAAGTGCTGATCCGCTGGCAGGCAGGG 2520
 2461 ACCTCCTGAACGAAAAGAACCGGAACGACTACGCTTACGACTAGGGGAGCCGTCCGCC
 CAGCTCCGGCGCTCCCGAGACCACTGCGCTCCACGTTGAGGTGGCGTGGGGGGCGGA 2580
 2521 GTCGAGGCCGCGAGGAGCCTCTGGTACCGAGGTGCAACTCCACCCGCACCCCCCGCCT
 CAGGAATTGAAGCGGAAGTCTGGAGCTTCTGGGCTGGAGGGGACCCCGTTGGA 2640
 2581 GTCCCTTAACCTCGCCTTCAGACCCCTCGAAATCCCAGCGACCTCCCCCTGGGCCAACCT

<---- 4.p53-BE ---->
 (intron)

2641 GAGAGGAGCGGAACCTCTGGACAAGCCCTGACAAGCCAAGCCAAAGGTCCGCTCCGGCGC 2700
 CTCTCCTCGCCTTGAGGACCTGTCGGACTGTTGGTCCGGTTCCAGGCAGGCCGCG

2701 GGGTGGGTGAGTGC CGCCGCCCCCGGGGGGGAGAGAGCCTACAGCCTCAGAACCA 2760
 CCCACCCACTACGCGCGGGCGCCCCCGCCCTCTCGGATGTCGAAGTCTTGT
 CATATTGCTCATTTCTGGCAGTTCTCAGACGTAGGAATAAGTCAGCACCGAACGAGTG 2820
 2761 GTATAACGAGTAAAGACCGTCAAGAGTCTGCATCCTTATTAGTCAGTCGGCTCGTCAC
 GTTAAGCCGGAGGGCTCGGAAGAACGGCACCTTTCTCGAAAAAGTTATATGGGGG 2880
 2821 CAATTCGGCCCTCCGAGCCTTCTTGCCGTGGAAAAGAAAGAGCTTTCAATATAACCCC
 CTGAATGAGCTTCTGGAGGCTTACCGTTTTTATTGTACACAGAAAAGGAAACTG 2940
 2881 GACTTACTCGAAGACCTCCGAACAAATGGAAAAATAACAGTGTGTCTTCCCTTGAC
 CCTTGTCTCCCTTCCGGAAATTCTCTTTAAAGACTGTAAGTCGCTGCCTGAGTGGTTTC 3000
 2941 GGAACAGAGGGAAGGCCCTTAAGAGAGAAATTCTGACATTCAAGGACGGACTCACAAAG
 ATTTTGTGTTCTGCCCTCTCTTTCTTCCCTTCTAGCTTGCACCTCC 3060
 3001 TAAAACAAACAAAAAGACGGGAAGAGAAAGAAAGAAACGGAAATCGAACGTGAGG
 CATGGTGATTCTGCTGGCTCCTGCTGGGGTTGGTGGTACTCGTCCCACCGCACAGA 3120
 3061 GTACCACTAAAGACGAACCGAGGGACGACCCCAACCACCATGAGCAAGGGTGGCGTGTCT
 ACCCGGCCCTATTATGGCCAAGAAACTTGAGCAGCTGTTGAAAAGTCCCTCGCTC 3180
 3121 TGGGCCGCGATAATAACCGGTTCTTGAACTCGTCGGACAAAACCTTCAGGGAGCGAG
 AGAAAATGCCAGCTTGAGATGGCTAATCAAAG 3212
 3181 TCTTACGGTCGAACGTCTACCGATTAGTTTC

Fig 11

variations in the p53 binding region of figure 8

1. p1140 IMI

p1140 GGACAAGCCCTGACAAGCCA

p1140 IMI **GGAAAAGCCCTGACAAGCCA**
 ↑

positions of the mutations (boldface and arrow): 2270 (C→A)

DRAFT
DRAFT
DRAFT
DRAFT
DRAFT
DRAFT
DRAFT
DRAFT

2. p1140 IMII

p1140 GGACAAGCCCTGACAAGCCA

p1140 IMII **GGAAAAGCCCTGAAAAGCCA**
 ↑ ↑

positions of the mutations (boldface and arrow): 2270 (C→A)

2280 (C→A)

3. p1140 IMIII

p1140 GGACAAGCCCTGACAAGCCA

p1140 IMIII **GGAAAATCCCTGAAAATCCA**
 ↑ ↑ ↑ ↑

positions of the mutations (boldface and arrow): 2270 (C→A)

2273 (G→T)

2280 (C→A)

2283 (G→T)

4. p1140 IMIV

p1140	GGACAAGCCCT G ACAAGCCA
p1140 IMIV	G CACAAGCCCT C ACAAGCCA
	↑ ↑

positions of the mutations (boldface and arrow): 2268 (G→T)

2278 (C→A)

Fig. 12

variations in the p53 binding regions of figure 9

1. p1141 IMIII

p1141	GGACAAGCCCTGACAAGCCA
p1141 IMIII	GGAAAATCCCTGAAATCCA
	↑↑↑↑

positions of the mutations (boldface and arrow): 2270

2273
2280
2283

2. p1141 1p53

p1141	AGAGATGCCAAACTGTTTT
p1141 1p53	AGAGATTCCCAAAATGTTTT
	↑↑

positions of the mutations (boldface and arrow): 50

57

3. p1141 2p53

p1141	AATGTTGCTTAAGCTTTTT
p1141 2p53	AATGTTCTTAAGATTTTT
	↑↑

positions of the mutations (boldface and arrow): 443

450

4. p1141 3p53

p1141	AAACTACCTAAGAGCTATCT
p1141 3p53	ACA ACTACCTAAGAGCTATCT
	↑↑

positions of the mutations (boldface and arrow): 1268 (A→C)
1270 (C→A)

5. p1141 ΔBgl

p1141	AATAACCTTT AGAGATGCCAAAC TGTTTCCCCAGAAC
p1141ΔBgl	AATAACCTTT A -----GATCTCCCCAGAAC

6. p1141 ΔSpe

p1141	CATCTTGCC ATGTTGCTTAAGCTTTTG GCTACATTT
p1141ΔBgl	CATCTTGCC A -----CTAGTGGCTACATTT

7. p1141 ΔMph

p1141	AATTCA TGCTAAACTACCTAAGAGCTATCT ACCGTTCCAA
p1141ΔBgl	AATTCA TGCTATGCA -----TACCGTTCCAA

variations in the p53 binding region of figure 10

1. p1142 TAG

mutation of the positions: 2227 (A→T)
2228 (T→A)

2. p1142 IMIII

p1142	GGACAAGCCCTGACAAGCCA
p1142 IMIII	GG AAA ATCCCTG AAA ATCCA
	↑↑↑↑

positions of the mutations (boldface and arrow): 2662 (C→A)

2665 (G→T)
2672 (C→A)
2675 (G→T)

3. p1142 ΔBgl

<---- 1.p53-BE ---->	
p1142	AATAAACCTTT AGAGATGCCA ACTGTTTCCCCAGAACCA
p1142ΔBgl	AATAAACCTTT A -----GATCTCCCCAGAACCA

4. p1142 ΔSpe

<---- 2.p53-BE ---->	
p1142	CATCTTGCC AATGTTGCTT AAGCTTTGGCTACATTT
p1142ΔBgl	CATCTTGCC A -----CTAGTGGCTACATTT

5. p1142 Δ Mph

p1142

p1142 Δ Bgl

<---- 3.p53-BE ---->

AATT CATGCT **AAACTACCTAAGAGCTATCTACCGTTCAA**
AATT CATGCT **ATGCA-----TACCGTTCAA**

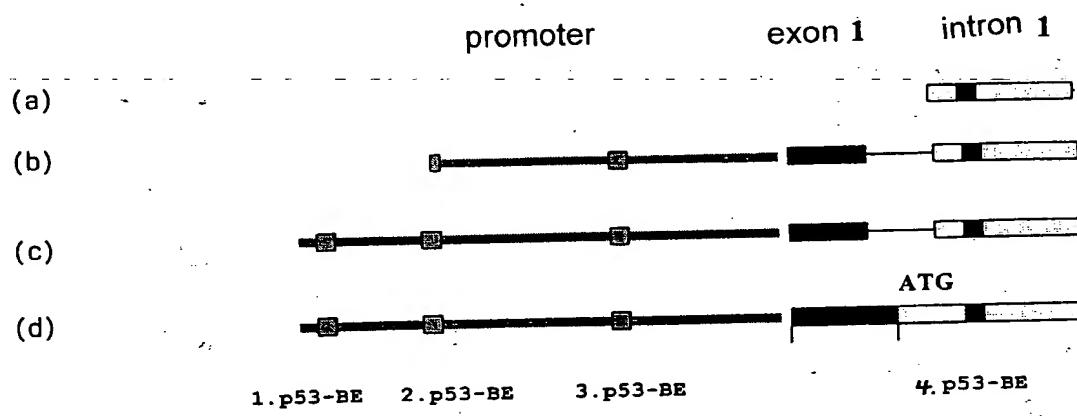


Fig. 14